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A new genus and species of freshwater mussel (Bivalvia, Unionidae) from Anhui, China

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Abstract

The middle and lower reaches of the Yangtze River host a highly diverse Unionidae fauna. Herein, a new genus and species of freshwater mussel, *Huizhou xietianxiangi* H. Chen, Z.-G. Chen, H.-Q. Xiang, Y.-M. He & X.-P. Wu, **gen. et sp. nov.**, is described from Huangshan City, Anhui Province, based on comparative morphological and molecular phylogenetic evidence. The new taxon is distinguished by a unique set of shell characteristics, including an oval shape, a zigzag sculpture covering the entire surface, and frequent adornment with elegant dark green rays. These distinct morphological features, coupled with significant genetic differentiation, robustly support its establishment as a new genus and species.

Key Words

Globunionini, Mollusca, phylogeny, taxonomy, Yangtze River Basin

Introduction

The Yangtze River Basin in China harbors a rich and endemic fauna of primary freshwater mussels, with more than 70 recognized species described to date (He and Zhuang 2013; Graf and Cummings 2021; Guo 2022; Dai et al. 2025). Recent extensive surveys and taxonomic studies have led to the continual discovery of new taxa (Chen et al. 2023; Dai et al. 2023, 2024a, b; Chen et al. 2025). Despite the numerous endemic species already documented, their full diversity remains incompletely understood, particularly among small-bodied forms, with even new tribes being identified (Dai et al. 2025). These findings indicate that a significant number of freshwater mussel species in the region have yet to be described.

In this study, researchers collected freshwater mussel specimens with distinctive shell morphology from Huangshan City, Anhui Province, China, which did not match any known species. Based on integrated morphological and molecular phylogenetic analyses, we describe it here as a new genus and new species within the subfamily Unioninae Rafinesque, 1820: *Huizhou xietianxiangi* sp. nov. This discovery further enriches the known freshwater mussel diversity of the Yangtze River Basin, particularly among the tiny fauna.

Materials and methods

Specimen sampling and morphological observations

Freshwater mussels were collected in the Xinanjiang River (29.5678°N, 117.9225°E), Bingtan Village, Xikou

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Town, Xiuning County, Huangshan City, Anhui Province, China, in August 2025 (Fig. 1). The specimens were preserved in 95% ethanol and deposited at the Museum of Biology, Nanchang University (NCUMB), China. A Vernier caliper was used to measure shell length (L), shell width (W), and shell height (H).

DNA extraction, PCR, sequencing, and phylogenetic analyses

Total genomic DNA was extracted from foot tissues using the TIANamp Marine Animals DNA Kit (Tiangen Biotech) following the manufacturer's protocol. F-type mitochondrial COI sequences were amplified using primers LCO22me2 (GGTCAACAAAYCATAARGATATTGG) and HCO700dy2 (TCAGGGTGACCAAAAAAYCA) (Walker et al. 2007). Polymerase chain reaction (PCR) amplifications of COI were performed in a final 25 μL reaction mixture containing 1 μL of template DNA, 1 μL of each primer, 12.5 μL of Green Taq Mix (Vazyme, China), and 9.5 μL of ddH_2O. Thermal cycling began with one cycle at 98 °C for 10 s, followed by 35 cycles of denaturation at 94 °C for 1 min, annealing at 50 °C for 1 min, and extension at 72 °C for 1 min, with a final extension at 72 °C for 7 min. The PCR products were purified and sequenced using an ABI 3730XL analyzer. The newly obtained sequences were deposited in GenBank (Table 1). Sequences were aligned using MAFFT v.7 based on the Q-INS-i method (Katoh et al. 2019). Pairwise distances between species were calculated using MEGA X (Kumar et al. 2018). The best substitution model was selected us-

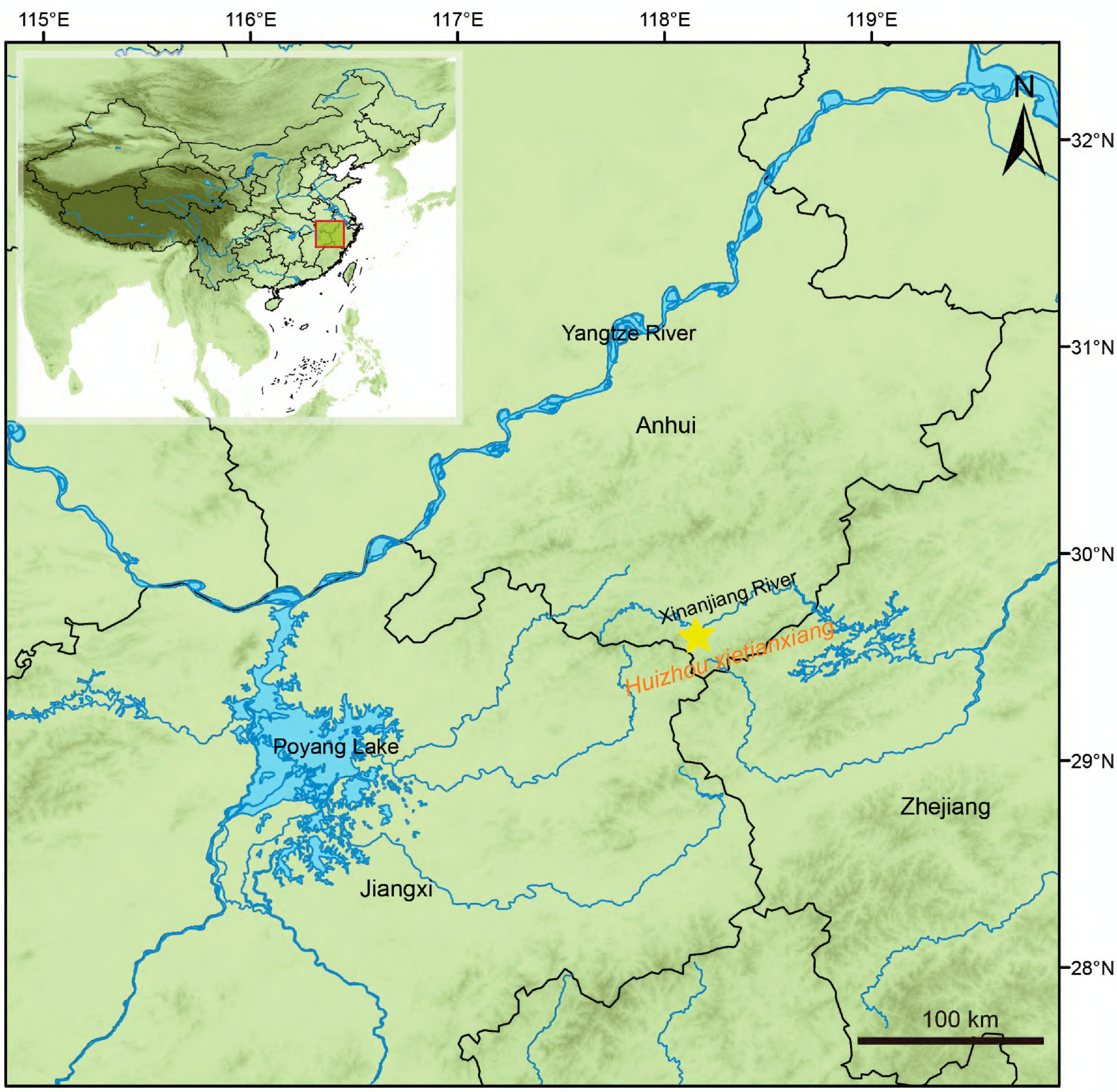

Figure 1. Collection sites of *Huizhou xietianxiangi* gen. et sp. nov. The gold star indicates the type locality.

Table 1. GenBank accession numbers of the COI sequences used in this study.

Species	Locality	Accession number
Huizhou xietianxiangi gen. et sp. nov.	Xiuning, Huangshan, Anhui, China	In submission
Huizhou xietianxiangi gen. et sp. nov.	Xiuning, Huangshan, Anhui, China	In submission
Globunio mirificus Chen, Dai, Huang & Wu, 2025	Nanchang, Jiangxi, China	PV368604
Globunio mirificus Chen, Dai, Huang & Wu, 2025	Nanchang, Jiangxi, China	PV368605
Diaurora aurorea (Heude, 1883)	Ji'an, Jiangxi, China	OQ829360
Acuticosta chinensis (Lea, 1868)	Jiangxi, China	MG462921
Schistodesmus lampreyanus (Baird & Adams, 1867)	Jiangxi, China	MG463037
Schistodesmus lampreyanus (Baird & Adams, 1867)	Hunan, China	MG463043
Schistodesmus spinosus (Simpson, 1900)	Jiangxi, China	MG463046
Unio pictorum (Linnaeus, 1758)	Europe	KC429109
Unio crassus Philipsson, 1788	Poland	KY290446
Tchangsinaia piscicula (Heude, 1874)	Jiangxi, China	MG462977
Cuneopsis celtiformis (Heude, 1874)	Jiangxi, China	MG462964
Cuneopsis heudei (Heude, 1874)	Jiangxi, China	MG462970
Aculamprotula fibrosa (Heude, 1877)	Jiangxi, China	MG462909
Nodularia douglasiae (Gray, 1833)	China	KX822653
Nodularia breviconcha Lee, Kim, Bogan & Kondo, 2020	South Korea	MT020662
Inversiunio yanagawensis (Kondo, 1982)	Japan	MT020654
Inversiunio reinianus (Kobelt, 1879)	Japan	MT020657
Pseudocuneopsis sichuanensis Huang, Dai, Chen & Wu, 2022	Sichuan, China	MZ540966
Pseudocuneopsis capitata (Heude, 1874)	Anhui, China	NC042469
Alasmidonta marginata Say, 1818	U.S.	AF156502
Lasmigona compressa (Lea, 1829)	U.S.	AF156503
Anodonta anatina (Linnaeus, 1758)	Russia	KX822632
Pseudanodonta complanata (Rossmässler, 1835)	Ukraine	KX822661
Lanceolaria gladiola (Heude, 1877)	Jiangxi, China	MG463007
Lanceolaria oxyrhyncha (Martens, 1861)	Japan	MT020648
Cristaria plicata (Leach, 1814)	Jiangxi, China	MG462956
Lepidodesma languilati (Heude, 1874)	Jiangxi, China	MG463015
Sinanodonta woodiana (Lea, 1834)	China	KX822668
Beringiana beringiana (Middendorff, 1851)	Japan	MT020557
*Plethol*ophus *tenuis* (Gray, 1833)	Vietnam	KX822658
Anemina arcaeformis (Heude, 1877)	Jiangxi, China	MG462936
Amuranodonta kijaensis Moskvicheva, 1973	Russia	MK574204
Coelatura aegyptiaca (Cailliaud, 1823)	Egypt	KJ081162
Indonaia andersoniana (Nevill, 1877)	Myanmar	MF352275
Parreysia nagpoorensis (Lea, 1860)	India	JQ861229
Pronodularia japanensis (Lea, 1859	Japan	LC505454
Lamprotula leaii (Gray, 1833)	Jiangxi, China	MG462996
Lampsilis siliquoidea (Barnes, 1823)	U.S.	MH560773
Quadrula quadrula (Rafinesque, 1820)	U.S.	HM230409
Margaritifera dahurica (Middendorff, 1850)	Russia	KJ161516
Gibbosula rochechouartii (Heude, 1875)	Jiangxi, China	MG463022

ing the corrected Bayesian Information Criterion (BIC) in MODELFINDER v.2.2.0 (Kalyaanamoorthy et al. 2017). Bayesian inference (BI) and maximum likelihood (ML) analyses were performed using MrBayes (ver. 3.2.6; Ronquist et al. 2012) and IQ-TREE (ver. 2.2; Minh et al. 2020), respectively, with reference to the selected model of sequence evolution. For Bayesian analysis, two runs were performed simultaneously with four Markov chains starting from a random tree. Bayesian posterior probabilities (BPPs) of nodes were determined using Metropolis-coupled Markov chains (one cold chain) for 2,000,000 generations, with sampling every 1000 generations. The first 25% of sampled trees were discarded as burn-in when the standard deviation of split frequencies between the two runs was less than 0.01; the remaining trees were then used to create a 50% majority-rule consensus tree and to estimate BPPs. Node support for maximum likelihood analysis was determined using 1000 rapid bootstrap (BS) replicates.

Results

The GTR+F+I+R4 model was selected as the best-fit model of nucleotide substitution by the AIC criterion. Molecular phylogenies based on BI and ML analyses

showed that the subfamily Unioninae formed a monophyletic group (BS = 85%, BPP = 0.94). The species collected from Huangshan, Anhui, China, together with *Globunio mirificus* Chen, Dai, Huang & Wu, 2025, formed a strongly supported monophyletic clade (BS = 86%, BPP = 0.92) (Figs 2, 3). Pairwise uncorrected COI p-distance analysis demonstrated a genetic distance of 11% between this species and *Globunio mirificus*. These distances, as well as the distinct morphological characteristics, provide compelling evidence for its classification as a new genus and species, *Huizhou xietianxiangi* sp. nov., in the tribe Globunionini.

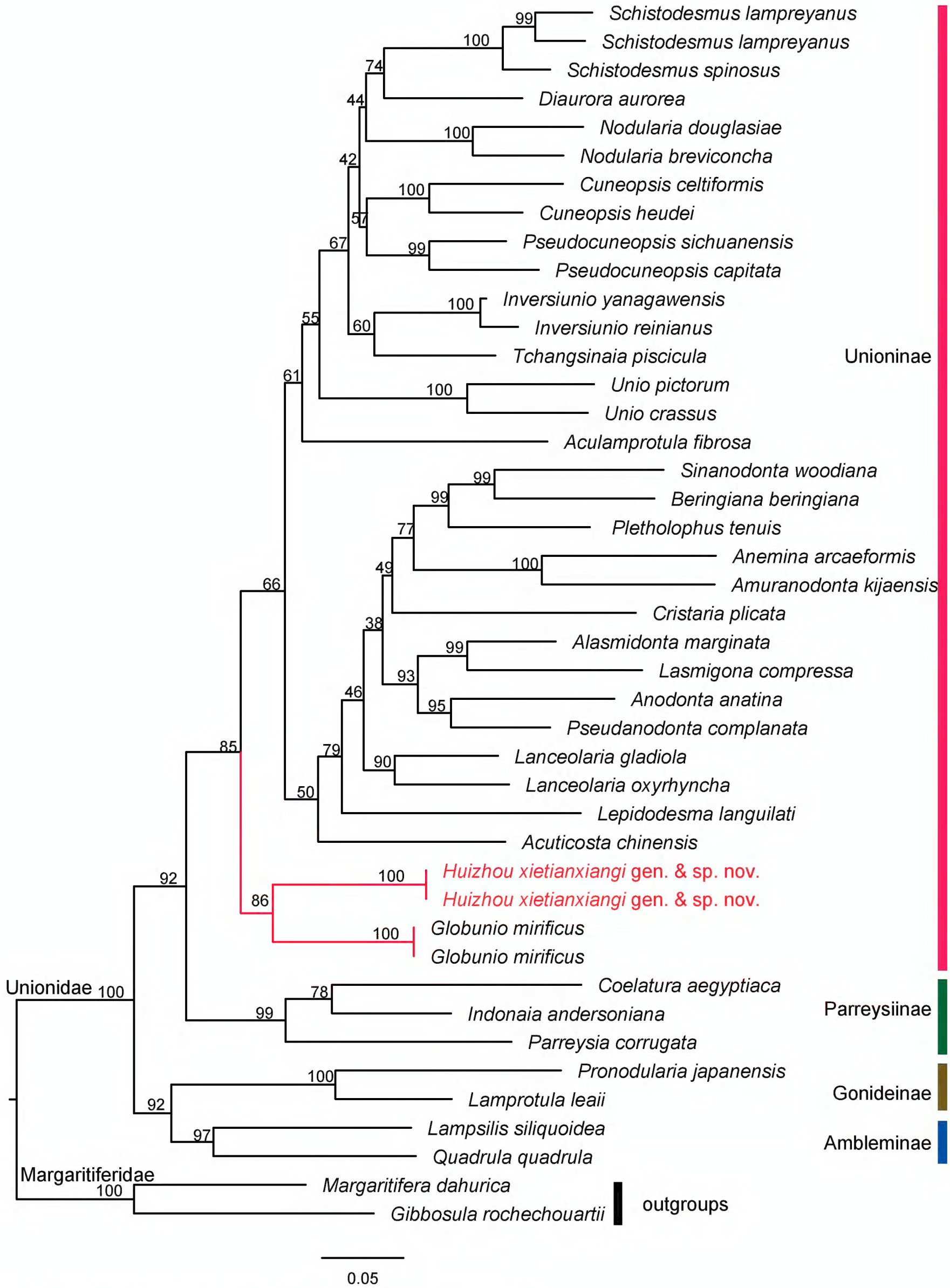

Figure 2. Maximum likelihood tree inferred from COI gene sequences.

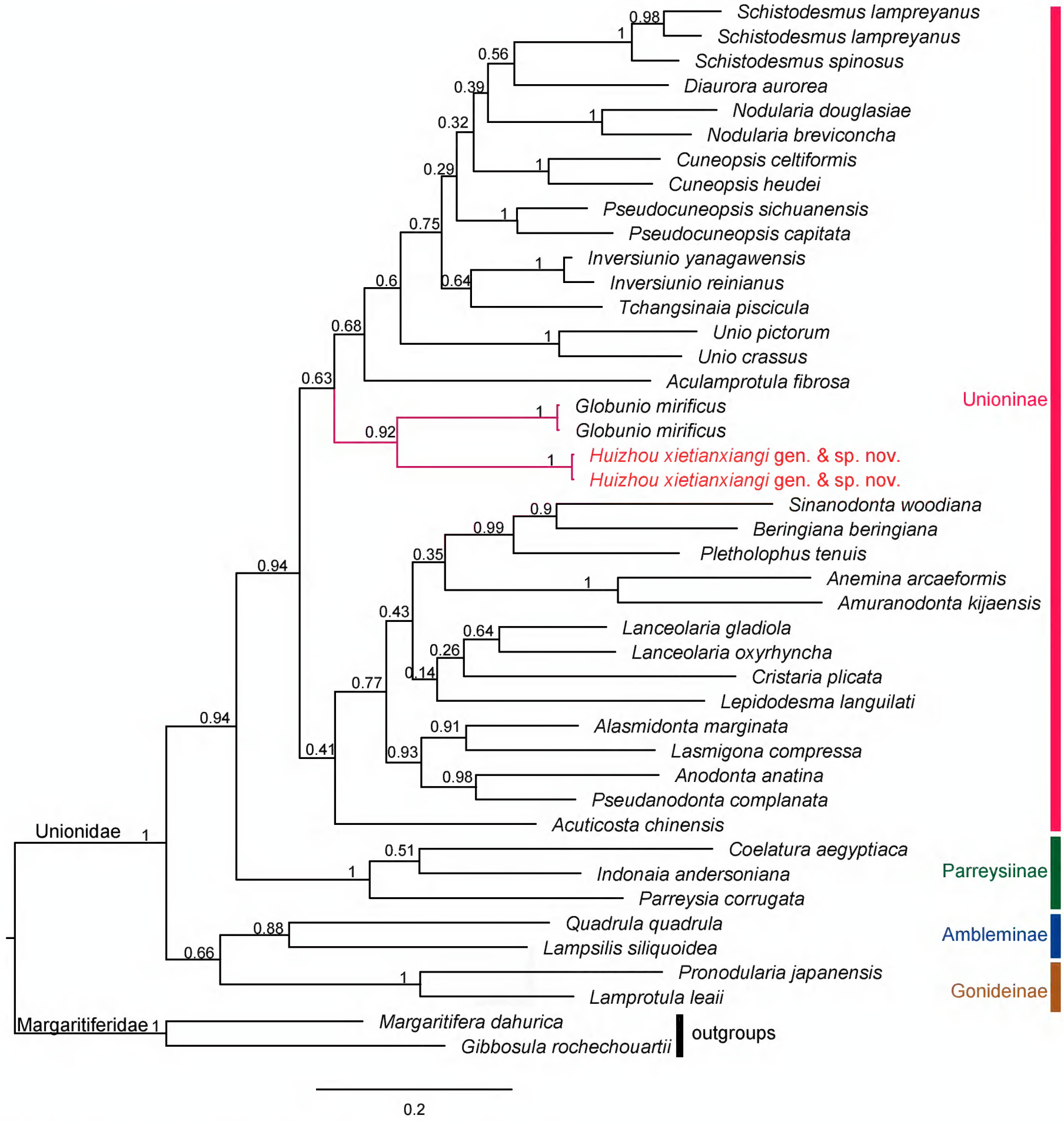

Figure 3. Bayesian inference tree inferred from COI gene sequences.

Systematics

Family Unionidae Rafinesque, 1820

Subfamily Unioninae Rafinesque, 1820

Tribe Globunionini Y.-T. Dai, Z.-G. Chen, X.-C. Huang & X.-P. Wu, 2025

Genus *Huizhou* H. Chen, Z.-G. Chen, H.-Q. Xiang, Y.-M. He & X.-P. Wu, gen. nov.

https://zoobank.org/0486F794-ADEB-46B5-8A00-94DBD10A0E5A

Type species. *Huizhou xietianxiangi* H. Chen, Z.-G. Chen, H.-Q. Xiang, Y.-M. He & X.-P. Wu, gen. et sp. nov. (Fig. 4).

Diagnosis. Shell small-sized, oval, thick, solid; with a zigzag sculpture covering the entire surface, often adorned with elegant dark green rays. Umbo inflated, often eroded. Incurrent aperture and excurrent aperture obvious papillae arranged in one row, excurrent aperture papillae are more than twice the size of the incurrent aperture.

Etymology. The name of this genus originates from the ancient Chinese place name Huizhou, which was an administrative region in Chinese history. The ancient name of the place where this species was discovered.

Vernacular name. 徽州蚌 (hui zhou bang). English common name: Huizhou Mussel.

Remarks. The establishment of the new genus *Huizhou* is justified by congruent evidence from morphology and molecular phylogeny. It differs morphologically from the type genus *Globunio* of the tribe Globunionini by lacking the diagnostic elongated-globular shell. Phylogenetically,

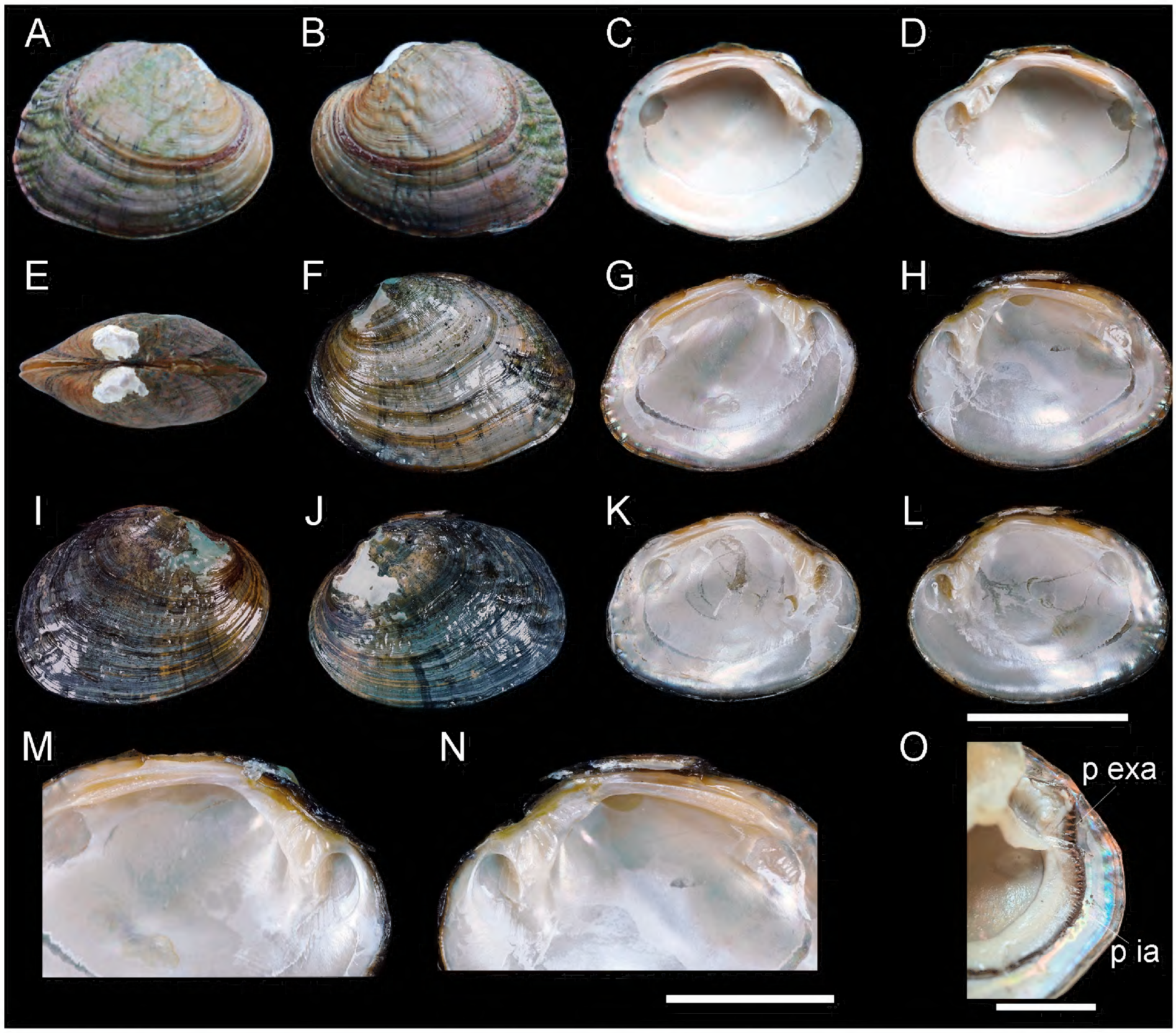

Figure 4. *Huizhou xietianxiangi* gen. et sp. nov. **A–E.** Holotype, NCUAH250801; **F–H.** Paratype, NCUAH250802; **I–L.** Paratype, NCUAH250803; **M, N.** Hinge structure of left and right valves; **O.** Anatomical features, *p ia*, papillae in incurrent aperture; *p exa*, papillae in excurrent aperture. Scale bars: 10 mm (**A–L**), 1 mm (**M, N**), 1 mm (**O**).

the two genera form distinct, strongly supported lineages with a considerable genetic distance (11% for COI), which falls within the range of intergeneric divergence observed in other unionid tribes. This combination of marked morphological discontinuity and significant genetic differentiation provides compelling evidence for their separation at the generic level.

***Huizhou xietianxiangi* H. Chen, Z.-G. Chen, H.-Q. Xiang, Y.-M. He & X.-P. Wu, sp. nov.**

https://zoobank.org/2DF41693-B63D-44BD-BE42-6AF3A2625A02

Material examined. ***Holotype*:** NCUAH250801, shell length 33.7 mm, shell width 14.7 mm, shell height 25.7 mm (Fig. 4A), Xinanjiang River, Bingtan Village, Xikou Town, Xiuning County, Huangshan City, Anhui Province, China, 29.5678°N, 117.9225°E, in August 2025.

***Paratypes*:** 2 specimens, NCUAH250802, 03; shell length 35.2, 33.5 mm; shell width 27.5, 25.1 mm; shell height 15.1, 13.8 mm; locality and habitat same as holotype.

Diagnosis. Same as the genus.

Description. Shell small-sized, oval, thick, solid; with a zigzag sculpture covering the entire surface but strengthening from umbo to edge, often adorned with elegant dark green rays. Umbo inflated, often eroded. Ligament short and strong. Mantle muscle scars obvious. Anterior adductor muscle scars oval, deep; posterior adductor muscle scars oval, shallow and smooth (Fig. 4A–L). Left valve with two pseudocardinal teeth, equal height; anterior pseudocardinal tooth of the right valve well developed, posterior pseudocardinal tooth reduced. Lateral teeth of both valves thick (Fig. 4M, N). Nacre white bluish-white. Incurrent aperture and excurrent apertures obvious papillae arranged in one row, excurrent aperture papillae are more than twice the size of the incurrent aperture, both aperture with brown pigmentation (Fig. 4O).

Figure 5. Habitats and live animals of *Huizhou xietianxiangi* gen. et sp. nov.

Etymology. The name of this species is in honor of Mr. Xie Tianxiang, a conchologist who collected the specimens.

Vernacular name. 谢氏徽州蚌 (Xie shi hui zhou bang). English common name: Xie's Huizhou Mussel.

Habitat and distribution. This species is currently only known to be distributed in the Xin'an River in Xiuning County, Huangshan City, Anhui Province (Figs 1, 5).

Discussion

The tribe Globunionini was recently established and previously included only *Globunio mirificus* (see Dai et al. 2025). In this study, through a combination of morphological and molecular phylogenetic analyses, we describe a new genus and species, *Huizhou xietianxiangi* gen. et sp. nov., from the Xinanjiang River in Anhui Province. The discovery of this second species provides critical independent support for the validity of the tribe Globunionini and confirms that it is not a monotypic lineage. This finding significantly enriches species diversity and enhances our understanding of the tribe's evolutionary history.

Similar to *G. mirificus*, *H. xietianxiangi* gen. et sp. nov. possesses a small and thick shell and occurs within the Yangtze River Basin (Dai et al. 2025). However, our findings reveal that *H. xietianxiangi* exhibits a considerably narrower distribution and is currently endemic to Anhui Province. This restricted range is particularly concerning given that numerous freshwater mussel species have been reported as endangered or extinct at the time of their discovery (Xiang et al. 2024, 2025). Although Anhui Province is recognized for its rich unionid diversity, the present study confirms that undescribed species, particularly small-bodied or cryptic taxa, likely remain overlooked. Therefore, we urge more detailed and systematic surveys in this region to identify such hidden diversity, ensuring that these species can be studied and afforded conservation priority before their habitats experience irreversible degradation.

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References

Chen ZG, Dai YT, Ouyang S, Huang XC, Wu XP (2023) Unveiling the identity of Diaurora Cockerell, 1903 (Bivalvia, Unionidae): Morphology, molecular phylogenetics, and the description of a new species. ZooKey3s 1173: 131–144. https://doi.org/10.3897/zookeys.1173.106148

Chen H, Xiang HQ, Dai YT, Chen ZG, He YM, Guo G, Wu XP, Huang XC (2025) A new genus and two new species of freshwater mussels

(Bivalvia, Unionidae) from Sichuan, China: Overlooked cryptic endemism in the upper Yangtze River Basin. Zoosystematics and Evolution 101(4): 1459–1470. https://doi.org/10.3897/zse.101.161018

Dai YT, Huang XC, Wu CHZ, Chen ZG, Guo L, Shu SY, Ouyang S, Wu XP (2023) Multilocus and mitogenomic phylogenetic analyses reveal a new genus and species of freshwater mussel (Bivalvia, Unionidae) from Guangxi, China. Invertebrate Systematics 37(2): 152–166. https://doi.org/10.1071/IS22048

Dai YT, Chen ZG, Peng KJ, Ouyang S, Huang XC, Wu XP (2024a) Revisiting the genus *Pseudocuneopsis* (Bivalvia, Unionidae): Morphology, mitochondrial phylogenomics, and the description of a new species. Zoologica Scripta 53: 323–337. https://doi.org/10.1111/zsc.12647

Dai YT, Chen ZG, Cheng YZ, Huang XC, Ouyang S, Shu FY, Wu XP (2024b) Molecular phylogeny reveals a new genus and species of freshwater mussel (Bivalvia, Unionidae, Gonideinae) from Jiangxi, China. Zoosystematics and Evolution 100(4): 1419–1429. https://doi.org/10.3897/zse.100.135217

Dai YT, Chen ZG, Li F, Ouyang S, Huang XC, Wu XP (2025) A new tribe, genus, and species of freshwater mussel from the Changjiang River Basin in China (Bivalvia, Unionidae, Unioninae). Zoosystematics and Evolution 101(2): 779–790. https://doi.org/10.3897/zse.101.151083

Graf DL, Cummings KS (2021) A 'big data' approach to global freshwater mussel diversity (Bivalvia: Unionoida), with an updated checklist of genera and species. The Journal of Molluscan Studies 87(2): eyaa034. https://doi.org/10.1093/mollus/eyab015

Guo L (2022) Unionoida. The Straits Publishing, China, 256 pp. [In Chinese]

He J, Zhuang ZM (2013) The Freshwater Bivalves of China. ConchBooks, Germany, 198 pp.

Kalyaanamoorthy S, Minh BQ, Wong TK, Von Haeseler A, Jermiin LS (2017) ModelFinder: Fast model selection for accurate phy logenetic estimates. Nature Methods 14: 587–589. https://doi.org/10.1038/nmeth.4285

Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: Multiple sequence alignment, interactive sequence choice and visu alization. Briefings in Bioinformatics 20(4): 1160–1166. https://doi.org/10.1093/bib/bbx108

Kumar S, Stecher G, Li M, Knyaz C, Tamura K (2018) MEGA X: Molecular evolutionary genetics analysis across computing platforms. Molecular Biology and Evolution 35(6): 1547–1549. https://doi.org/10.1093/molbev/msy096

Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, Lanfear R (2020) IQ-TREE 2: New models and efficient methods for phylogenetic infer ence in the genomic era. Molecular Biology and Evolution 37(5): 1530–1534. https://doi.org/10.1093/molbev/msaa015

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Walker JM, Bogan AE, Bonfiglio EA, Campbell DC, Christian AD, Curole JP, Harris JL, Wo jtecki RJ, Hoeh WR (2007) Primers for amplifying the hypervariable, male-transmitted COII–COI junction region in amblemine freshwater mussels (Bivalvia: Unionoidea: Ambleminae). Molecular Ecology Notes 7(3): 489–491. https://doi.org/10.1111/j.1471-8286.2006.01630.x

Xiang HQ, He YM, Zhang LJ, Gao H, Guo L, Lu YZ, Fan SY, Chen H (2024) A revision of *Rhombuniopsis* Haas, 1920 (Unionida, Unionidae) endemic to the ancient lakes of Yunnan, China, with descriptions of two new species. Zootaxa 5481(2): 273–289. https://doi.org/10.11646/zootaxa.5481.2.6

Xiang HQ, Lu YZ, He YM, Li CY (2025) A new genus and two new species of freshwater mussel Unioninae (Bivalvia: Unionida) endemic to Yunnan of SW China. The Indochina Entomologist 1(30): 289–304. https://doi.org/10.70590/ice.2025.01.30